

1. US-09-895-814-17 Sequence 172, Application 159 159 6.51 0

4 100% similar sequences to the query sequence were found:

Sequence Name	Description	Length	Score	Sig.	Frame
2. US-09-895-814-61 Sequence 617, Application 449 159 159 6.51 0					
3. US-09-895-814-52 Sequence 525, Application 254 159 159 6.51 0					

1. US-09-895-814-172 (1-159)  
US-09-895-814-17 Sequence 172, Application US/09895814

Initial Score = 159 Optimized Score = 159 Significance = 6.51  
Residue Identity = 100% Matches = 159 Mismatches = 0  
Gaps = 0 Conservative Substitutions

2. US-09-895-814-172 (1-159)  
US-09-895-814-61 Sequence 617, Application US/09895814

Initial Score = 159 Optimized Score = 159 Significance = 6.51  
Residue Identity = 98% Matches = 157 Mismatches = 2  
Gaps = 0 Conservative Substitutions

3. US-09-895-814-172 (1-159)  
US-09-895-814-52 Sequence 525, Application US/09895814

Initial Score = 159 Optimized Score = 159 Significance = 6.51  
Residue Identity = 98% Matches = 157 Mismatches = 2  
Gaps = 0 Conservative Substitutions

1. US-09-895-814-172 (1-159)  
US-09-895-814-17 Sequence 172, Application US/09895814

Initial Score = 159 Optimized Score = 159 Significance = 6.51  
Residue Identity = 100% Matches = 159 Mismatches = 0  
Gaps = 0 Conservative Substitutions

2. US-09-895-814-172 (1-159)  
US-09-895-814-61 Sequence 617, Application US/09895814

Initial Score = 159 Optimized Score = 159 Significance = 6.51  
Residue Identity = 98% Matches = 157 Mismatches = 2  
Gaps = 0 Conservative Substitutions

3. US-09-895-814-172 (1-159)  
US-09-895-814-52 Sequence 525, Application US/09895814

Initial Score = 159 Optimized Score = 159 Significance = 6.51  
Residue Identity = 98% Matches = 157 Mismatches = 2  
Gaps = 0 Conservative Substitutions

X 10 20  
MVEASLSVRHPEYNRPPLANDL  
|||||  
AALVNEELFCGVLVHPQWVLSAAHCFQNSYTTIGLHLSLEADQEPGQSMVEASLSVRHPEYNRPPLANDL  
50 60 70 80 90 100 110  
X 100  
30 40 50 60 70 80 90  
MLIKLDESVSSEDTIRISISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEEVCSKLYDPLHPS  
|||||  
MLIKLDESVSSEDTIRISISIASQCPTAGNSCLVSGWGLLANGRMPTVLQCVNVSVVSEEVCSKLYDPLHPS  
120 130 140 150 160 170 180  
100 110 120 130 140 150 X  
MFCAGGGQXQXDSNCGDSGGFLICNGYLQGLVSEFGKAPCGQGVPGVYTNLCKFTEWIEKTVQAS  
|||||  
MFCAGGGQXQXDSNCGDSGGFLICNGYLQGLVSEFGKAPCGQGVPGVYTNLCKFTEWIEKTVQAS  
190 200 210 220 230 240 250 X